



PCT

RAW SEQUENCE LISTING

DATE: 07/17/2003

PATENT APPLICATION: US/09/763,822A

TIME: 11:32:33

Input Set : A:\W0008463.txt

Output Set: N:\CRF4\07172003\I763822A.raw

ENTERED

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3 <110> APPLICANT: WALLAART, Thorvald Eelco
4   BOUWMEESTER, Hendrik Jan
6 <120> TITLE OF INVENTION: Transgenic Amorpha-4, 11-Diene Synthesis
8 <130> FILE REFERENCE: 702 010272
10 <140> CURRENT APPLICATION NUMBER: 09/763,822A
C--> 11 <141> CURRENT FILING DATE: 2003-05-05
13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/06302
14 <151> PRIOR FILING DATE: 1999-08-27
16 <160> NUMBER OF SEQ ID NOS: 14
18 <170> SOFTWARE: MS Word 97 SR-2
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21 <211> LENGTH: 15
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: EcoR I (Not I) adapter
28 <400> SEQUENCE: 1
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32 <211> LENGTH: 19
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: EcoR I (Not I) adapter
39 <400> SEQUENCE: 2
40 cagctgcgcc gccgcttaa                                     19
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 27
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Sense primer (primer C) used in PCR amplification
50 <400> SEQUENCE: 3
51 gtcgacaaac catggcactt acagaag                             27
53 <210> SEQ ID NO: 4
54 <211> LENGTH: 32
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Antisense primer (primer D) used in PCR amplification
61 <400> SEQUENCE: 4
62 ggatggatcc tcatatactc ataggataaa cg                       32
64 <210> SEQ ID NO: 5

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65 <211> LENGTH: 23
66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Sense primer (primer G) used in PCR amplification
72 <400> SEQUENCE: 5
73 gaggatccat gtcacttaca gaa                                23
75 <210> SEQ ID NO: 6
76 <211> LENGTH: 24
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Antisense primer (primer H) used in PCR amplification
83 <400> SEQUENCE: 6
84 atggatcctc atatactcat agga                                24
86 <210> SEQ ID NO: 7
87 <211> LENGTH: 22
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Sense primer (primer E) used in PCR amplification
94 <400> SEQUENCE: 7
95 cgagaattca tgtcacttac ag                                22
97 <210> SEQ ID NO: 8
98 <211> LENGTH: 22
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Antisense primer (primer F) used in PCR amplification
105 <400> SEQUENCE: 8
106 ggatctcgag tcatatactc at                                22
108 <210> SEQ ID NO: 9
109 <211> LENGTH: 538
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Nucleotide sequence of probe generated by PCR with primers A
115     and B
117 <400> SEQUENCE: 9
118 gatgagaatg ggaaatttaa ggaatcgta gctaataatg ttgaagggtt gcttgagttg    60
120 tacgaagcaa cttctatgag ggtacctggg gagattatat tagaagatgc tcttggtttt    120
122 acacgatctc gtcttagcat tatgacaaaa gatgcttttt ctacaaaccc cgctcttttt    180
124 accgaaatac aacgggcact aaagcaaccc ctttggaataa ggttgccaag aatagaggcg    240
126 gcgcagtaca ttcctttcta tcaacaacaa gattctcata acaagacttt acttaactt    300
128 gctaagttag agttcaattt gcttcagtca ttgcacaagg aagagctcag ccatgtgtgc    360
130 aaatggtgga aagctttcga tatcaagaag aacgcacctt gttaagaga tagaattggt    420
132 gaatgctact tttggggact aggttcaggc tatgagccac agtattcccg ggctagagtt    480
134 ttcttcacaa aagctgttgc tgttataact cttatagacg acaccttcga cgctacgg    538
136 <210> SEQ ID NO: 10

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TIME: 11:32:33

Input Set : A:\W0008463.txt

Output Set: N:\CRF4\07172003\I763822A.raw

137 <211> LENGTH: 179

138 <212> TYPE: PRT

139 <213> ORGANISM: Artificial Sequence

141 <220> FEATURE:

142 <223> OTHER INFORMATION: Deduced amino acid sequence of probe generated by PCR with
143 primers A and B

145 <400> SEQUENCE: 10

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147 1 5 10 15

148 Leu Leu Glu Leu Tyr Glu Ala Thr Ser Met Arg Val Pro Gly Glu Ile

149 20 25 30

150 Ile Leu Glu Asp Ala Leu Gly Phe Thr Arg Ser Arg Leu Ser Ile Met

151 35 40 45

152 Thr Lys Asp Ala Phe Ser Thr Asn Pro Ala Leu Phe Thr Glu Ile Gln

153 50 55 60

154 Arg Ala Leu Lys Gln Pro Leu Trp Lys Arg Leu Pro Arg Ile Glu Ala

155 65 70 75 80

156 Ala Gln Tyr Ile Pro Phe Tyr Gln Gln Gln Asp Ser His Asn Lys Thr

157 85 90 95

158 Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Leu Leu Gln Ser Leu His

159 100 105 110

160 Lys Glu Glu Leu Ser His Val Cys Lys Trp Trp Lys Ala Phe Asp Ile

161 115 120 125

162 Lys Lys Asn Ala Pro Cys Leu Arg Asp Arg Ile Val Glu Cys Tyr Phe

163 130 135 140

164 Trp Gly Leu Gly Ser Gly Tyr Glu Pro Gln Tyr Ser Arg Ala Arg Val

165 145 150 155 160

166 Phe Phe Thr Lys Ala Val Ala Val Ile Thr Leu Ile Asp Asp Thr Phe

167 165 170 175

168 Asp Ala Thr

170 <210> SEQ ID NO: 11

171 <211> LENGTH: 2112

172 <212> TYPE: DNA

173 <213> ORGANISM: Artemisia annua L.

175 <220> FEATURE:

176 <223> OTHER INFORMATION: Nucleotide sequence of a positive clone (amorphadiene
synthase

177 encoding gene) isolated from the cDNA library of induced A.annua

179 <400> SEQUENCE: 11

180 aattcgcggc cgcgtcgaca aatcatgtca cttacagaag aaaaacctat tcgccccatt 60

182 gccaactttc ctccaagcat ttggggagat cagtttctca tctatcaaaa gcaagtagag 120

184 caaggggtgg aacagatagt gaatgattta aaaaaagaag tgcggcaact actaaaagaa 180

186 gctttggata ttctatgaa acatgccaat ttgttgaagc tgattgatga aattcaacgc 240

188 cttggaatac cgtatcactt tgaacgggag attgatcatg cattgcaatg tatttatgaa 300

190 acatatggtg ataactggaa tggtagaccgc tcttccttat ggttccgtct tatgcgaaag 360

192 caaggatatt atgttacatg tgatgttttc aataactata aagacaaaaa tggagcggtc 420

194 aagcaatcgt tagctaatga tgttgaaggt ttgcttgagt tgtacgaagc aacttctatg 480

196 agggtagctg gggagattat attagaagat gctcttggtt ttacacgata tcgtcttagc 540

198 attatgacaa aagatgcttt ttctacaaac cccgctcttt ttaccgaaat acaacgggca 600

200 ctaaagcaac ccctttggaa aaggttgcca agaataagag cgcgcgagta cattcctttc 660

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202 tatcaacaac aagattctca taacaagact ttacttaaac ttgctaagtt agagttcaat 720
204 ttgcttcagt cattgcacaa ggaagagctc agccatgtgt gcaaagtgtg gaaagctttc 780
206 gatatcaaga agaacgcacc ttgtttaaga gatagaattg ttgaatgcta cttttgggga 840
208 ctaggttcag gctatgagcc acagtattcc cgggctagag ttttcttcac aaaagctggt 900
210 gctgttataa ctcttataga tgacacttat gatgcgtatg gtacttatga agaacttaag 960
212 atctttactg aagctgttga aaggtggtca attacatgct tagacacact tccagaatac 1020
214 atgaaaccga tatacaaat attcatggat acatacacag aaatggaaga atttcttgca 1080
216 aaggaggga gaacagatct atttaactgc ggcaaagaat ttgtgaaaga gtttggtaga 1140
218 aacctgatgg ttgaagcaaa atgggcaa atgggacaca taccaaccac tgaagagcat 1200
220 gatccagttg taatcattac tggcgtgct aacctgctta caacaacttg ttatcttggc 1260
222 atgagtata tattcacaaa agagtctgtc gaatgggctg tctctgcacc tcctctttt 1320
224 agatactcag gtatacttg tcgacgccta aatgatctca tgaccacaa ggccgagcaa 1380
226 gaaagaaaa atagttcatc gagccttgaa agttatatga aggaatataa tgtcaatgag 1440
228 gagtatgcc aaaccttgat ttacaaggaa gtagaagatg tgtggaaaga tataaaccga 1500
230 gagtaccca caactaaaaa cattccaagg ccgttattga tggctgtgat ctatttgtgc 1560
232 cagtttcttg aagtcaata tgcaggaaa gataacttca cacgtatggg agacgaatac 1620
234 aaacatctca taaagtctct actcgtttat cctatgagta tatgactacc aatccttcgt 1680
236 gcatagccta tcaattatat tgaagggtt aactatgcac gtctctatgg agagaatttc 1740
238 tcaagctatt tgggtgttct tgctggcaat aataaatcag acgcataaaa ttgtattgaa 1800
240 ctatatgccg atagctattt aaagttatta tacaactaaa atattcaaca atggtattat 1860
242 acttttactt tgtacaaaag caaaagtaca ctactgttat gtaacatttt agttctatga 1920
244 tactttagtt acgaatcggc ttatatacat tgatacact ttatgcagaa aaccctagta 1980
246 aataaaaaagt cgatatcttg tactacacat atcgacgaa ttccggttg ccgtttgtat 2040
248 tttacgatat gttatttaat gaatatgttt catgtggttg ttgcttaaaa aaaaagtcga 2100
250 cgcggccgcg aa 2112

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252 <210> SEQ ID NO: 12

253 <211> LENGTH: 697

254 <212> TYPE: PRT

255 <213> ORGANISM: Artemisia annua L.

257 <220> FEATURE:

258 <223> OTHER INFORMATION: Deduced amino acid sequence of a positive clone
(amorphadiene

259 synthase encoding gene) isolated from the cDNA library of

260 induced A.annua

262 <400> SEQUENCE: 12

263 Asn Ser Arg Pro Arg Arg Gln Ile Met Ser Leu Thr Glu Glu Lys Pro

264 1 5 10 15

265 Ile Arg Pro Ile Ala Asn Phe Pro Pro Ser Ile Trp Gly Asp Gln Phe

266 20 25 30

267 Leu Ile Tyr Gln Lys Gln Val Glu Gln Gly Val Glu Gln Ile Val Asn

268 35 40 45

269 Asp Leu Lys Lys Glu Val Arg Gln Leu Leu Lys Glu Ala Leu Asp Ile

270 50 55 60

271 Pro Met Lys His Ala Asn Leu Leu Lys Leu Ile Asp Glu Ile Gln Arg

272 65 70 75 80

273 Leu Gly Ile Pro Tyr His Phe Glu Arg Glu Ile Asp His Ala Leu Gln

274 85 90 95

275 Cys Ile Tyr Glu Thr Tyr Gly Asp Asn Trp Asn Gly Asp Arg Ser Ser

276 100 105 110

277 Leu Trp Phe Arg Leu Met Arg Lys Gln Gly Tyr Tyr Val Thr Cys Asp

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278          115          120          125
279 Val Phe Asn Asn Tyr Lys Asp Lys Asn Gly Ala Phe Lys Gln Ser Leu
280          130          135          140
281 Ala Asn Asp Val Glu Gly Leu Leu Glu Leu Tyr Glu Ala Thr Ser Met
282 145          150          155          160
283 Arg Val Pro Gly Glu Ile Ile Leu Glu Asp Ala Leu Gly Phe Thr Arg
284          165          170          175
285 Ser Arg Leu Ser Ile Met Thr Lys Asp Ala Phe Ser Thr Asn Pro Ala
286          180          185          190
287 Leu Phe Thr Glu Ile Gln Arg Ala Leu Lys Gln Pro Leu Trp Lys Arg
288          195          200          205
289 Leu Pro Arg Ile Glu Ala Ala Gln Tyr Ile Pro Phe Tyr Gln Gln Gln
290          210          215          220
291 Asp Ser His Asn Lys Thr Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn
292 225          230          235          240
293 Leu Leu Gln Ser Leu His Lys Glu Glu Leu Ser His Val Cys Lys Trp
294          245          250          255
295 Trp Lys Ala Phe Asp Ile Lys Lys Asn Ala Pro Cys Leu Arg Asp Arg
296          260          265          270
297 Ile Val Glu Cys Tyr Phe Trp Gly Leu Gly Ser Gly Tyr Glu Pro Gln
298          275          280          285
299 Tyr Ser Arg Ala Arg Val Phe Thr Lys Ala Val Ala Val Ile Thr
300          290          295          300
301 Leu Ile Asp Asp Thr Tyr Asp Ala Tyr Gly Thr Tyr Glu Glu Leu Lys
302 305          310          315          320
303 Ile Phe Thr Glu Ala Val Glu Arg Trp Ser Ile Thr Cys Leu Asp Thr
304          325          330          335
305 Leu Pro Glu Tyr Met Lys Pro Ile Tyr Lys Leu Phe Met Asp Thr Tyr
306          340          345          350
307 Thr Glu Met Glu Glu Phe Leu Ala Lys Glu Gly Arg Thr Asp Leu Phe
308          355          360          365
309 Asn Cys Gly Lys Glu Phe Val Lys Glu Phe Val Arg Asn Leu Met Val
310          370          375          380
311 Glu Ala Lys Trp Ala Asn Glu Gly His Ile Pro Thr Thr Glu Glu His
312 385          390          395          400
313 Asp Pro Val Val Ile Ile Thr Gly Gly Ala Asn Leu Leu Thr Thr Thr
314          405          410          415
315 Cys Tyr Leu Gly Met Ser Asp Ile Phe Thr Lys Glu Ser Val Glu Trp
316          420          425          430
317 Ala Val Ser Ala Pro Pro Leu Phe Arg Tyr Ser Gly Ile Leu Gly Arg
318          435          440          445
319 Arg Leu Asn Asp Leu Met Thr His Lys Ala Glu Gln Glu Arg Lys His
320          450          455          460
321 Ser Ser Ser Ser Leu Glu Ser Tyr Met Lys Glu Tyr Asn Val Asn Glu
322 465          470          475          480
323 Glu Tyr Ala Gln Thr Leu Ile Tyr Lys Glu Val Glu Asp Val Trp Lys
324          485          490          495
325 Asp Ile Asn Arg Glu Tyr Leu Thr Thr Lys Asn Ile Pro Arg Pro Leu
326          500          505          510

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VERIFICATION SUMMARY

DATE: 07/17/2003

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Input Set : A:\W0008463.txt

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

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<110> WALLAART, Thorvald Eelco
BOUWMEESTER, Hendrik Jan

<120> Transgenic Amorpha-4, 11-Diene Synthesis

<130> 702 010272

<140> 09/763,822

<141> 2001-02-26

<150> PCT/EP99/06302

<151> 1999-08-27

<160> 14

<170> MS Word 97 SR-2

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<213> Artificial Sequence

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<223> EcoR I (Not I) adapter

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15

<210> 2

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> EcoR I (Not I) adapter

<400> 2

cagctgcgcc ggcgcttaa

19

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Sense primer (primer C) used in PCR amplification

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27

<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>
 <223> Antisense primer (primer D) used in PCR amplification

 <400> 4
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 <210> 5
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sense primer (primer G) used in PCR amplification

 <400> 5
 gaggatccat gtcacttaca gaa 23

 <210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Antisense primer (primer H) used in PCR amplification

 <400> 6
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 <210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sense primer (primer E) used in PCR amplification

 <400> 7
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 <210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Antisense primer (primer F) used in PCR amplification

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 <210> 9
 <211> 538
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nucleotide sequence of probe generated by PCR with primers A

and B

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acacgatctc gtcttagcat tatgacaaaa gatgcttttt ctacaaaccc cgctcttttt      180
accgaaatac aacgggcact aaagcaaccc ctttggaata gggtgccaag aatagaggcg      240
gcgcagtaca ttcttttcta tcaacaacaa gattctcata acaagacttt acttaaactt      300
gctaagttag agttcaattt gcttcagtca ttgcacaagg aagagctcag ccatgtgtgc      360
aaatggtgga aagctttcga tatcaagaag aacgcacctt gttaagaga tagaattggt      420
gaatgctact tttggggact aggttcaggc tatgagccac agtattcccg ggctagagtt      480
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<210> 10

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Deduced amino acid sequence of probe generated by PCR with
primers A and B

<400> 10

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Leu Leu Glu Leu Tyr Glu Ala Thr Ser Met Arg Val Pro Gly Glu Ile
 20          25          30
Ile Leu Glu Asp Ala Leu Gly Phe Thr Arg Ser Arg Leu Ser Ile Met
 35          40          45
Thr Lys Asp Ala Phe Ser Thr Asn Pro Ala Leu Phe Thr Glu Ile Gln
 50          55          60
Arg Ala Leu Lys Gln Pro Leu Trp Lys Arg Leu Pro Arg Ile Glu Ala
 65          70          75          80
Ala Gln Tyr Ile Pro Phe Tyr Gln Gln Gln Asp Ser His Asn Lys Thr
 85          90          95
Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Leu Leu Gln Ser Leu His
100          105          110
Lys Glu Glu Leu Ser His Val Cys Lys Trp Trp Lys Ala Phe Asp Ile
115          120          125
Lys Lys Asn Ala Pro Cys Leu Arg Asp Arg Ile Val Glu Cys Tyr Phe
130          135          140
Trp Gly Leu Gly Ser Gly Tyr Glu Pro Gln Tyr Ser Arg Ala Arg Val
145          150          155          160
Phe Phe Thr Lys Ala Val Ala Val Ile Thr Leu Ile Asp Asp Thr Phe
165          170          175
Asp Ala Thr
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<210> 11

<211> 2112

<212> DNA

<213> *Artemisia annua* L.

<220>

<223> Nucleotide sequence of a positive clone (amorphadiene synthase encoding gene) isolated from the cDNA library of induced *A.annua*

<400> 11

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caaggggttg aacagatagt gaatgattta aaaaaagaag tgcggcaact actaaaagaa    180
gctttggata ttcctatgaa acatgccaat ttgttgaagc tgattgatga aattcaacgc    240
cttgaatac cgtatcactt tgaacgggag attgatcatg cattgcaatg tatttatgaa    300
acatatggtg ataactggaa tggtgaccgc tcttccttat ggttccgtct tatgcgaaag    360
caaggatatt atgttacatg tgatgttttc aataactata aagacaaaaa tggagcgttc    420
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ctaaagcaac ccctttggaa aagggttgcca agaataagagg cggcgcagta cattcctttc    660
tatcaacaac aagattctca taacaagact ttacttaaac ttgctaagtt agagttcaat    720
ttgcttcagt cattgcacaa ggaagagctc agccatgtgt gcaaattggtg gaaagctttc    780
gatatcaaga agaacgcacc ttgtttaaga gatagaattg ttgaatgcta cttttgggga    840
ctaggttcag gctatgagcc acagtattcc cgggctagag ttttcttcac aaaagctggt    900
gctgttataa ctcttataga tgacacttat gatgcgtatg gtacttatga agaacttaag    960
atctttactg aagctgttga aagggtgtca attacatgct tagacacact tccagaatac   1020
atgaaaccga tatacaaatt attcatggat acatacacag aaatggaaga atttcttgca   1080
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agatactcag gtatacttgg tcgacgccta aatgatctca tgaccacaaa ggccgagcaa   1380
gaaagaaaac atagttcatc gagccttgaa agttatatga aggaatataa tgtcaatgag   1440
gagtatgccc aaaccttgat ttacaaggaa gtagaagatg tgtggaaaga tataaaccga   1500
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gagtacctca caactaaaaa cattccaagg ccgttattga tggctgtgat ctatttgtgc 1560
cagtttcttg aagttcaata tgcaggaaag gataacttca cacgtatggg agacgaatac 1620
aaacatctca taaagtctct actcgtttat cctatgagta tatgactacc aatccttcgt 1680
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tacttttagtt acgaatcggc ttatatacat tgatacactt ttatgcagaa aaccctagta 1980
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<210> 12

<211> 697

<212> PRT

<213> *Artemisia annua* L.

<220>

<223> Deduced amino acid sequence of a positive clone (amorphadiene synthase encoding gene) isolated from the cDNA library of induced *A.annua*

<400> 12

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 1           5           10           15
Ile Arg Pro Ile Ala Asn Phe Pro Pro Ser Ile Trp Gly Asp Gln Phe
      20           25           30
Leu Ile Tyr Gln Lys Gln Val Glu Gln Gly Val Glu Gln Ile Val Asn
      35           40           45
Asp Leu Lys Lys Glu Val Arg Gln Leu Leu Lys Glu Ala Leu Asp Ile
      50           55           60
Pro Met Lys His Ala Asn Leu Leu Lys Leu Ile Asp Glu Ile Gln Arg
      65           70           75           80
Leu Gly Ile Pro Tyr His Phe Glu Arg Glu Ile Asp His Ala Leu Gln
      85           90           95
Cys Ile Tyr Glu Thr Tyr Gly Asp Asn Trp Asn Gly Asp Arg Ser Ser
      100          105          110
Leu Trp Phe Arg Leu Met Arg Lys Gln Gly Tyr Tyr Val Thr Cys Asp
      115          120          125
Val Phe Asn Asn Tyr Lys Asp Lys Asn Gly Ala Phe Lys Gln Ser Leu
      130          135          140
Ala Asn Asp Val Glu Gly Leu Leu Glu Leu Tyr Glu Ala Thr Ser Met
      145          150          155          160
Arg Val Pro Gly Glu Ile Ile Leu Glu Asp Ala Leu Gly Phe Thr Arg
      165          170          175
Ser Arg Leu Ser Ile Met Thr Lys Asp Ala Phe Ser Thr Asn Pro Ala

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			180					185				190					
Leu	Phe	Thr	Glu	Ile	Gln	Arg	Ala	Leu	Lys	Gln	Pro	Leu	Trp	Lys	Arg		
		195					200					205					
Leu	Pro	Arg	Ile	Glu	Ala	Ala	Gln	Tyr	Ile	Pro	Phe	Tyr	Gln	Gln	Gln		
	210					215					220						
Asp	Ser	His	Asn	Lys	Thr	Leu	Leu	Lys	Leu	Ala	Lys	Leu	Glu	Phe	Asn		
225					230					235					240		
Leu	Leu	Gln	Ser	Leu	His	Lys	Glu	Glu	Leu	Ser	His	Val	Cys	Lys	Trp		
			245						250					255			
Trp	Lys	Ala	Phe	Asp	Ile	Lys	Lys	Asn	Ala	Pro	Cys	Leu	Arg	Asp	Arg		
		260						265					270				
Ile	Val	Glu	Cys	Tyr	Phe	Trp	Gly	Leu	Gly	Ser	Gly	Tyr	Glu	Pro	Gln		
	275						280					285					
Tyr	Ser	Arg	Ala	Arg	Val	Phe	Phe	Thr	Lys	Ala	Val	Ala	Val	Ile	Thr		
	290					295					300						
Leu	Ile	Asp	Asp	Thr	Tyr	Asp	Ala	Tyr	Gly	Thr	Tyr	Glu	Glu	Leu	Lys		
305					310					315					320		
Ile	Phe	Thr	Glu	Ala	Val	Glu	Arg	Trp	Ser	Ile	Thr	Cys	Leu	Asp	Thr		
			325					330						335			
Leu	Pro	Glu	Tyr	Met	Lys	Pro	Ile	Tyr	Lys	Leu	Phe	Met	Asp	Thr	Tyr		
			340					345					350				
Thr	Glu	Met	Glu	Glu	Phe	Leu	Ala	Lys	Glu	Gly	Arg	Thr	Asp	Leu	Phe		
	355					360						365					
Asn	Cys	Gly	Lys	Glu	Phe	Val	Lys	Glu	Phe	Val	Arg	Asn	Leu	Met	Val		
	370					375					380						
Glu	Ala	Lys	Trp	Ala	Asn	Glu	Gly	His	Ile	Pro	Thr	Thr	Glu	Glu	His		
385					390					395					400		
Asp	Pro	Val	Val	Ile	Ile	Thr	Gly	Gly	Ala	Asn	Leu	Leu	Thr	Thr	Thr		
			405					410						415			
Cys	Tyr	Leu	Gly	Met	Ser	Asp	Ile	Phe	Thr	Lys	Glu	Ser	Val	Glu	Trp		
		420						425					430				
Ala	Val	Ser	Ala	Pro	Pro	Leu	Phe	Arg	Tyr	Ser	Gly	Ile	Leu	Gly	Arg		
	435					440						445					
Arg	Leu	Asn	Asp	Leu	Met	Thr	His	Lys	Ala	Glu	Gln	Glu	Arg	Lys	His		
	450					455					460						
Ser	Ser	Ser	Ser	Leu	Glu	Ser	Tyr	Met	Lys	Glu	Tyr	Asn	Val	Asn	Glu		
465					470					475					480		
Glu	Tyr	Ala	Gln	Thr	Leu	Ile	Tyr	Lys	Glu	Val	Glu	Asp	Val	Trp	Lys		
			485					490						495			
Asp	Ile	Asn	Arg	Glu	Tyr	Leu	Thr	Thr	Lys	Asn	Ile	Pro	Arg	Pro	Leu		
		500						505					510				
Leu	Met	Ala	Val	Ile	Tyr	Leu	Cys	Gln	Phe	Leu	Glu	Val	Gln	Tyr	Ala		
	515						520					525					
Gly	Lys	Asp	Asn	Phe	Thr	Arg	Met	Gly	Asp	Glu	Tyr	Lys	His	Leu	Ile		
	530					535					540						
Lys	Ser	Leu	Leu	Val	Tyr	Pro	Met	Ser	Ile	Leu	Pro	Ile	Leu	Arg	Ala		
545					550					555					560		
Pro	Ile	Asn	Tyr	Ile	Glu	Arg	Val	Asn	Tyr	Ala	Arg	Leu	Tyr	Gly	Glu		
			565					570						575			
Asn	Phe	Ser	Ser	Tyr	Leu	Val	Phe	Leu	Ala	Gly	Asn	Asn	Lys	Ser	Asp		
		580						585					590				
Ala	Asn	Cys	Ile	Glu	Leu	Tyr	Ala	Asp	Ser	Tyr	Leu	Lys	Leu	Leu	Tyr		
	595					600					605						
Asn	Asn	Ile	Gln	Gln	Trp	Tyr	Tyr	Thr	Phe	Thr	Leu	Tyr	Lys	Ser	Lys		
	610					615					620						
Ser	Thr	Leu	Leu	Leu	Cys	Asn	Ile	Leu	Val	Leu	Tyr	Phe	Ser	Tyr	Glu		
625					630					635					640		

Ser Ala Tyr Ile His Tyr Thr Phe Met Gln Lys Thr Leu Val Asn Lys
645 650 655
Lys Ser Ile Ser Cys Thr Thr His Ile Ala Arg Ile Ser Val Cys g
660 665 670
Leu Tyr Phe Thr Ile Cys Tyr Leu Met Asn Met Phe His Val Val Val
675 680 685
Ala Lys Lys Ser Arg Arg Gly Arg Glu
690 695

<210> 13

<211> 1649

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the amorphadiene synthase encoding gene,
between start and stop codon, obtained by PCR with primers C
and D

<400> 13

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ccatggcact tacagaagaa aaacctattc gccccattgc caactttcct ccaagcattt    60
ggggagatca gtttctcatc tatcaaaagc aagtagagca aggggtggaa cagatagtga    120
atgatttaaa aaaagaagtg cggcaactac taaaagaagc tttggatatt cctatgaaac    180
atgccaatTTt gttgaagctg attgatgaaa ttcaacgcct tggaataccg tatcactttg    240
aacgggagat tgatcatgca ttgcaatgta tttatgaaac atatggtgat aactggaatg    300
gtgaccgctc ttccttatgg ttccgtctta tgcgaaagca aggatattat gttacatgtg    360
atgttttcaa taactataaa gacaaaaatg gagcgttcaa gcaatcgta gctaattgatg    420
ttgaaggttt gcttgagttg tacgaagcaa cttctatgag ggtacctggg gagattatat    480
tagaagatgc tcttggtttt acacgatctc gtcttagcat tatgacaaaa gatgcttttt    540
ctacaaaccc cgctcttttt accgaaatac aacgggcact aaagcaaccc ctttggaaaa    600
ggttgccaag aatagaggcg gcgcagtaca ttcctttcta tcaacaaca gattctcata    660
acaagacttt acttaaactt gctaagttag agttcaattt gcttcagtca ttgcacaagg    720
aagagctcag ccatgtgtgc aaatggtgga aagctttcga tatcaagaag aacgcacctt    780
gtttaagaga tagaattggt gaatgctact tttggggact aggttcaggc tatgagccac    840
agtattcccg ggctagagtt ttcttcacaa aagctgttgc tgttataact cttatagatg    900
acacttatga tgcgtatggt acttatgaag aacttaagat ctttactgaa gctgttgaaa    960
ggtggtcaat tacatgctta gacacacttc cagaatacat gaaaccgata tacaattat    1020
tcatggatac atacacagaa atggaagaat ttcttgcaaa ggagggaaga acagatctat    1080
ttaactgcgg caaagaattt gtgaaagagt ttgtagaaa cctgatggtt gaagcaaaat    1140
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gggcaaata gggacacata ccaaccactg aagagcatga tccagttgta atcattactg 1200
gcggtgctaa cctgcttaca acaacttggt atcttggcat gagtgatata ttcacaaaag 1260
agtctgtcga atgggctgtc tctgcacctc ctcttttttag atactcaggt atacttggtc 1320
gacgcctaaa tgatctcatg acccacaagg cggagcaaga aagaaaacat agttcatcga 1380
gccttgaaag ttatatgaag gaatataatg tcaatgagga gtatgcccaa accttgattt 1440
acaaggaagt agaagatgtg tggaaagata taaaccgaga gtacctcaca actaaaaaca 1500
ttccaaggcc gttattgatg gctgtgatct atttgtgcc gtttcttgaa gttcaatatg 1560
caggaaagga taacttcaca cgtatgggag acgaatacaa acatctcata aagtctctac 1620
tcgtttatcc tatgagtata tgaggatcc 1649

```

<210> 14

<211> 549

<212> PRT

<213> Artificial Sequence

<220>

<223> Deduced amino acid sequence of the amorphadiene synthase
encoding gene, between start and stop codon, obtained by PCR
with primers C and D

<400> 14

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Thr Met Ala Leu Thr Glu Glu Lys Pro Ile Arg Pro Ile Ala Asn Phe
      5              10              15
Pro Pro Ser Ile Trp Gly Asp Gln Phe Leu Ile Tyr Gln Lys Gln Val
      20              25              30
Glu Gln Gly Val Glu Gln Ile Val Asn Asp Leu Lys Lys Glu Val Arg
      35              40              45
Gln Leu Leu Lys Glu Ala Leu Asp Ile Pro Met Lys His Ala Asn Leu
      50              55              60
Leu Lys Leu Ile Asp Glu Ile Gln Arg Leu Gly Ile Pro Tyr His Phe
      65              70              75              80
Glu Arg Glu Ile Asp His Ala Leu Gln Cys Ile Tyr Glu Thr Tyr Gly
      85              90              95
Asp Asn Trp Asn Gly Asp Arg Ser Ser Leu Trp Phe Arg Leu Met Arg
      100             105             110
Lys Gln Gly Tyr Tyr Val Thr Cys Asp Val Phe Asn Asn Tyr Lys Asp
      115             120             125
Lys Asn Gly Ala Phe Lys Gln Ser Leu Ala Asn Asp Val Glu Gly Leu
      130             135             140
Leu Glu Leu Tyr Glu Ala Thr Ser Met Arg Val Pro Gly Glu Ile Ile
      145             150             155             160
Leu Glu Asp Ala Leu Gly Phe Thr Arg Ser Arg Leu Ser Ile Met Thr
      165             170             175
Lys Asp Ala Phe Ser Thr Asn Pro Ala Leu Phe Thr Glu Ile Gln Arg
      180             185             190
Ala Leu Lys Gln Pro Leu Trp Lys Arg Leu Pro Arg Ile Glu Ala Ala
      195             200             205
Gln Tyr Ile Pro Phe Tyr Gln Gln Gln Asp Ser His Asn Lys Thr Leu

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210		215		220
Leu Lys Leu Ala Lys	Leu Glu Phe Asn Leu	Leu Leu Gln Ser Leu	His Lys	
225	230	235	240	
Glu Glu Leu Ser His	Val Cys Lys Trp Trp	Lys Ala Phe Asp Ile Lys		
	245	250	255	
Lys Asn Ala Pro Cys	Leu Arg Asp Arg	Ile Val Glu Cys Tyr Phe Trp		
	260	265	270	
Gly Leu Gly Ser Gly	Tyr Glu Pro Gln Tyr Ser	Arg Ala Arg Val Phe		
	275	280	285	
Phe Thr Lys Ala Val	Ala Val Ile Thr Leu Ile	Asp Asp Thr Tyr Asp		
	290	295	300	
Ala Tyr Gly Thr Tyr	Glu Glu Leu Lys Ile	Phe Thr Glu Ala Val Glu		
305	310	315	320	
Arg Trp Ser Ile Thr	Cys Leu Asp Thr Leu	Pro Glu Tyr Met Lys Pro		
	325	330	335	
Ile Tyr Lys Leu Phe	Met Asp Thr Tyr Thr	Glu Met Glu Glu Phe Leu		
	340	345	350	
Ala Lys Glu Gly Arg	Thr Asp Leu Phe Asn Cys	Gly Lys Glu Phe Val		
	355	360	365	
Lys Glu Phe Val Arg	Asn Leu Met Val Glu	Ala Lys Trp Ala Asn Glu		
	370	375	380	
Gly His Ile Pro Thr	Thr Glu Glu His Asp	Pro Val Val Ile Ile Thr		
385	390	395	400	
Gly Gly Ala Asn Leu	Thr Thr Thr Cys Tyr	Leu Gly Met Ser Asp		
	405	410	415	
Ile Phe Thr Lys Glu	Ser Val Glu Trp Ala	Val Ser Ala Pro Pro Leu		
	420	425	430	
Phe Arg Tyr Ser Gly	Ile Leu Gly Arg Arg	Leu Asn Asp Leu Met Thr		
	435	440	445	
His Lys Ala Glu Gln	Glu Arg Lys His Ser	Ser Ser Ser Leu Glu Ser		
	450	455	460	
Tyr Met Lys Glu Tyr	Asn Val Asn Glu Glu	Tyr Ala Gln Thr Leu Ile		
465	470	475	480	
Tyr Lys Glu Val Glu	Asp Val Trp Lys Asp	Ile Asn Arg Glu Tyr Leu		
	485	490	495	
Thr Thr Lys Asn Ile	Pro Arg Pro Leu Leu	Met Ala Val Ile Tyr Leu		
	500	505	510	
Cys Gln Phe Leu Glu	Val Gln Tyr Ala Gly	Lys Asp Asn Phe Thr Arg		
	515	520	525	
Met Gly Asp Glu Tyr	Lys His Leu Ile Lys	Ser Leu Leu Val Tyr Pro		
	530	535	540	
Met Ser Ile Gly Ser				
545				